

**Amendments to the Specification:**

Please replace paragraph 0074 with the following amended paragraph:

Conventional Techniques for Obtaining Genomic Data: A number of conventional approaches for obtaining genomic data over the Internet are available, some of which are described in the book edited by Ouelette and Bzevanis, incorporated by reference above. Figure 3 is a functional block diagram representing one simplified example. As shown in Figure 3, user 101 may consult any of a number of public or other sources to obtain accession numbers 224'. As represented by manual operation 312, user 101 initiates request 312 by accessing through any web browser the Internet web site of the National Center for Biotechnology Information (NCBI) of the National Library of Medicine and the National Institutes of Health (~~as of November 2002, accessible at the Internet URL <http://www.ncbi.nlm.nih.gov/>~~). In particular, user 101 may access the Entrez search and retrieval system that provides information from various databases at NCBI. These databases provide information regarding nucleotide sequences, protein sequences, macromolecular structures, whole genomes, and publication data related thereto. It is illustratively assumed that user 101 accesses in this manner NCBI Entrez nucleotide database 314 and receives information including gene or EST sequences 316. Particularly if accession numbers 224' represents a large number (e.g., one hundred) of EST's or genes of interest, as may easily be the case following analysis of probe array experiments, the tasks thus far described may take significant time, perhaps hours.

Please replace paragraph 0076 with the following amended paragraph:

User 101 typically copies sequence information from sequences 316 and pastes this information into an HTML document accessible through NCBI's BLAST web pages 324 (~~as of November 2002, accessible at <http://www.ncbi.nlm.nih.gov/BLAST/>~~). This operation, which also may be time consuming and tedious if many sequences are involved, is represented by user-initiated batch BLAST request 322 of Figure 3. BLAST is an acronym for Basic Local Alignment Search Tool, and, as is well known in the art, consists of similarity search programs that interrogate sequence databases for both protein and DNA using heuristic algorithms to seek local alignments. For example, user 101 may conduct a BLAST search using the "blastn" nucleotide sequence database. Results of this batch BLAST search, represented by similar nucleotide and/or protein sequence data 326, on occasion may not be available to user 101 for many minutes or even hours. User 101 may then initiate comparisons and evaluations 332, which may be conducted manually or using various software tools. User 101 may subsequently issue report 334 interpreting the findings of the searches and positing strategies and requirements for follow-on experiments.

Please replace paragraph 0142 with the following amended paragraph:

In some implementations, field 1510 may include names of catalog arrays, i.e., arrays previously designed and/or manufactured and stocked for shipment, that include an indicated subset (i.e., an indicated percentage and/or list) of the probe sets of interest to the user. For example, in response to a user's request for design of probe sets or probe arrays corresponding to user-selected probe set identifiers, gene or EST verifier 1110

determines verified probe sets, as described above. Gene or EST verifier 1110 may also send a query to database manager 512 to determine which of the verified probe sets already exist on catalog arrays, a database of which may be included in local products database 514. Database manager 512 may send information specifying the identified catalog array or arrays to user data processor 840 that may then enable presentation of this information to the user via an appropriate graphical user interface. Thus, for example, the user may be notified by entries in custom probe array display field 1510 that specified probe sets responsive to the user's request are already included in specified catalog arrays. The user may select the identified catalog array and, for example, also select accept button 1540 to indicate a desire to order the selected catalog array. In the manner described below, shipping, price, and other information related to the ordering and shipment of the catalog array may be displayed to the user in production information display field 1530. One of many examples of catalog arrays is the Human Genome U133 Set available from Affymetrix, Inc. ~~Other catalog arrays from Affymetrix are listed, as of November 2002, at <http://www.affymetrix.com/products/arrays/index.affx>.~~ A custom array may become a catalog array such as, for example, when a user consents that the custom array be made available to other users. Similarly a custom array may become a made-to-order array, which is an array that, like a catalog array, typically is listed for general sale but, unlike a catalog array, typically is not stocked for rapid shipment and instead is made to order.